REMARKS

Specification Amendment:

The specification has been amended to delete references to certain primers disclosed elsewhere and not essential to the claimed subject matter. Accordingly, the application no longer contains nucleotide and/or amino sequences. No new matter has been added by this amendment.

Sequence Listing Requirements:

The above amendment, deleting nucleotide sequences from the Specification, obviates the necessity for a Sequence Listing. Accordingly, 37 C.F.R. §§1.821 through 1.825 no longer apply.

Withdrawal of the requirement for a Sequence Listing is therefore requested.

Conclusions:

Applicants submit that the application is now fully in condition for examination.

Early and favorable examination on the merits is hereby requested.

Respectfully submitted,

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APPENDIX - VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE SPECIFICATION

The paragraph beginning at page 14, line 26 and ending at page 15, line 30 has been amended as follows:

Cells at various times postinfection were harvested and resuspended in ice cold TNE (10 mM Tris [pH 7.8], 150 mM NaCl, 1 mM EDTA) to which NP-40 was then added to a final concentration of 1%. After 5 minutes, the nuclei were pelleted and RNA was extracted from the supernatant using the phenol:chloroform procedure. Equal amounts of total cellular RNA from each sample were then subjected to RT-PCR (Wong, H.[,] et al., (1994) Anal. Biochem.[,] 223:251-258) using random hexanucleotide primers (Pharmacia) and RTase (GIBCO-BRL) according to the manufacturers' protocol. [The cDNA's from the RT-PCR step was then subjected to the selective amplification of reovirus s1 cDNA using the primer 5'-AATTCGATTTAGGTGACACTATAGCTATTGGTCGGATG-3' (SEQ ID NO:1) and 5'-CCCTTTTGACAGTGATGCTCCGTTATCACTCG-3' (SEQ ID NO:2) that amplify a predicted 116 bp fragment. These primer sequences were derived from the S1 sequence determined previously (Nagata, L. et al., (1984) Nucleic Acids Res. 12:8699-8710). The GAPDH primers (Wong, H., et al., (1994) Anal. Biochem., 223:251-258), 5'-CGGAGTCAACGGATTTGGTCGTAT-3' (SEQ ID NO:3) and 5'-AGCCTTCTCCATGGTGGTGAAGAC-3' (SEQ ID NO:4) were used to amplify a predicted 306 bp GAPDH fragment which served as a PCR and gel loading control.] The cDNAs from the RT-PCR step were then subjected to selective amplification of reovirus

cDNA using appropriate primers that amplify a predicted 116 bp fragment. These primer sequences were derived from the S1 sequence determined previously (Nagata, L. *et al.*, (1984) *Nucleic Acids Res. 12*:8699-8710). The GAPDH primers of Wong, H. *et al.*, (1994) Anal. Biochem. *223*:251-258 were used to amplify a predicted 306 bp GAPDH fragment which served as a PCR and gel loading control. Selective amplification of the s1 and GAPDH cDNA's was performed using Taq DNA polymerase (GIBCO-BRL) according to the manufacturers' protocol using a Perkin Elmer Gene Amp PCR system 9600. PCR was carried out for 28 cycles with each consisting of a denaturing step for 30 seconds at 97°C, annealing step for 45 seconds at 55°C, and polymerization step for 60 seconds at 72°C. PCR products were analyzed by electrophoresis through an ethidium bromide-impregnated TAE-2% agarose gel and photographed under ultra-violet illumination with Polaroid 57 film.